

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: NI, JIAN
GENTZ, REINER L.
RUBEN, STEVEN M.
- (ii) TITLE OF INVENTION: T1 RECEPTOR-LIKE LIGAND II
- (iii) NUMBER OF SEQUENCES: 25
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
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 - (C) CITY: WASHINGTON
 - (D) STATE: D.C.
 - (E) COUNTRY: USA
 - (F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US To be assigned
 - (B) FILING DATE: Herewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/024,348
 - (B) FILING DATE: 23-AUG-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: STEFFE, ERIC K.
 - (B) REGISTRATION NUMBER: 36,688
 - (C) REFERENCE/DOCKET NUMBER: 1488.0390001/EKS/AJK
- (ix) TELECOMMUNICATION INFORMATION:
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 - (B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1244 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 55..741
- (ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 55..130

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 133..741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CACGAGGACA ACAGTACCTG ACGCCTCTTT CAGCCC GGGA TCGCCCCAGC AGGG ATG	57
Met	
-26	
GGC GAC AAG ATC TGG CTG CCC TTC CCC GTG CTC CTT CTG GCC GCT CTG	105
Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala Leu	
-25 -20 -15 -10	
CCT CCG GTG CTG CTG CCT GGG GCG GCC GGC TTC ACA CCT TCC CTC GAT	153
Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu Asp	
-5 1 5	
AGC GAC TTC ACC TTT ACC CTT CCC GCC GGC CAG AAG GAG TGC TTC TAC	201
Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe Tyr	
10 15 20	
CAG CCC ATG CCC CTG AAG GCC TCG CTG GAG ATC GAG TAC CAA GTT TTA	249
Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val Leu	
25 30 35	
GAT GGA GCA GGA TTA GAT ATT GAT TTC CAT CTT GCC TCT CCA GAA GGC	297
Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu Gly	
40 45 50 55	
AAA ACC TTA GTT TTT GAA CAA AGA AAA TCA GAT GGA GTT CAC ACT GTA	345
Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr Val	
60 65 70	
GAG ACT GAA GTT GGT GAT TAC ATG TTC TGC TTT GAC AAT ACA TTC AGC	393
Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe Ser	
75 80 85	
ACC ATT TCT GAG AAG GTG ATT TTC TTT GAA TTA ATC CTG GAT AAT ATG	441
Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu Asp Asn Met	
90 95 100	
GGA GAA CAG GCA CAA GAA CAA GAA GAT TGG AAG AAA TAT ATT ACT GGC	489
Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly	
105 110 115	
ACA GAT ATA TTG GAT ATG AAA CTG GAA GAC ATC CTG GAA TCC ATC AAC	537
Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Glu Ser Ile Asn	
120 125 130 135	
AGC ATC AAG TCC AGA CTA AGC AAA AGT GGG CAC ATA CAA ACT CTG CTT	585
Ser Ile Lys Ser Arg Leu Ser Lys Ser Gly His Ile Gln Thr Leu Leu	
140 145 150	
AGA GCA TTT GAA GCT CGT GAT CGA AAC ATA CAA GAA AGC AAC TTT GAT	633
Arg Ala Phe Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp	
155 160 165	

AGA GTC AAT TTC TGG TCT ATG GTT AAT TTA GTG GTC ATG GTG GTG GTG	681
Arg Val Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val Val	
170 175 180	
TCA GCC ATT CAA GTT TAT ATG CTG AAG AGT CTG TTT GAA GAT AAG AGG	729
Ser Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys Arg	
185 190 195	
AAA AGT AGA ACT TAAACTCCA AACTAGAGTA CGTAACATTG AAAAATGAGG	781
Lys Ser Arg Thr	
200	
CATAAAAAATG CCATAAACTG TTACAGTCCA GACCATTAAT GGTCTTCTCC AAAATATTTT	841
GAGATATAAA AGTAGGAAAC AGGTATAATT TTAATGTGAA AATTAAGTCT TCACTTTCTG	901
TGCAAGTAAT CCTGCTGATC CAGTTGTACT TAAGTGTGTA ACAGGAATAT TTTGCAGAAT	961
ATAGGTTTAA CTGAATGAAG CCATATTAAT AACTGCATTT TCCTAACTTT GAAAAATTTT	1021
GCAAATGTCT TAGGTGATTT AAATAAATGA GTATTGGGCC TAATTGCAAC ACCAGTCTGT	1081
TTTTAACAGG TTCTATTACC CAGAACTTTT TTGTAAATGC GGCAGTTACA AATTAAGTGT	1141
GGAAGTTTTC AGTTTAAAGT TATAAATCAC CTGAGAATTA CCTAATGATG GATTGAATAA	1201
ATCTTTAGAC TACAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA	1244

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala	
-26 -25 -20 -15	
Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu	
-10 -5 1 5	
Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe	
10 15 20	
Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val	
25 30 35	
Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu	
40 45 50	
Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr	
55 60 65 70	
Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe	
75 80 85	
Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu Asp Asn	

90	95	100
Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr 105 110 115		
Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Glu Ser Ile 120 125 130		
Asn Ser Ile Lys Ser Arg Leu Ser Lys Ser Gly His Ile Gln Thr Leu 135 140 145 150		
Leu Arg Ala Phe Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe 155 160 165		
Asp Arg Val Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val 170 175 180		
Val Ser Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys 185 190 195		
Arg Lys Ser Arg Thr 200		

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 227 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Met Ala Ala Gly Ala Ala Leu Ala Leu Ala Leu Trp Leu Leu Met 1 5 10 15
Pro Pro Val Glu Val Gly Gly Ala Gly Pro Pro Pro Ile Gln Asp Gly 20 25 30
Glu Phe Thr Phe Leu Leu Pro Ala Gly Arg Lys Gln Cys Phe Tyr Gln 35 40 45
Ser Ala Pro Ala Asn Ala Ser Leu Glu Thr Glu Tyr Gln Val Ile Gly 50 55 60
Gly Ala Gly Leu Asp Val Asp Phe Thr Leu Glu Ser Pro Gln Gly Val 65 70 75 80
Leu Leu Val Ser Glu Ser Arg Lys Ala Asp Gly Val His Thr Val Glu 85 90 95
Pro Thr Glu Ala Gly Asp Tyr Lys Leu Cys Phe Asp Asn Ser Phe Ser 100 105 110
Thr Ile Ser Glu Lys Leu Val Phe Phe Glu Leu Ile Phe Asp Ser Leu 115 120 125

Gln Asp Asp Glu Glu Val Glu Gly Trp Ala Glu Ala Val Glu Pro Glu
 130 135 140
 Glu Met Leu Asp Val Lys Met Glu Asp Ile Lys Glu Ser Ile Glu Thr
 145 150 155 160
 Met Arg Thr Arg Leu Glu Arg Ser Ile Gln Met Leu Thr Leu Leu Arg
 165 170 175
 Ala Phe Glu Ala Arg Asp Arg Asn Leu Gln Glu Gly Asn Leu Glu Arg
 180 185 190
 Val Asn Phe Trp Ser Ala Val Asn Val Ala Val Leu Leu Leu Val Ala
 195 200 205
 Val Leu Gln Val Cys Thr Leu Lys Arg Phe Phe Gln Asp Lys Arg Pro
 210 215 220
 Val Pro Thr
 225

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGCCCATGGC CGGCTTCACA CCTTCC

26

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGCAAGCTTT CATCTATCAA AGTTGCTTTC

30

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGCGGATCCG CCATCATGGG CGACAAGATC TGG

33

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGCGGTACCT CACAATGTTA CGTACTCTAG

30

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGCGGTACCT CATCTATCAA AGTTGCTTTC

30

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGCTCTAGAT CAAGCGTAGT CTGGGACGTC GTATGGGTAT CTATCAAAGT TGCTTTC

57

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGACAGAGGG ACTTTCCGAG AGGA

24

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AATTCGGCAC GAGCTTCTAC CAGCCCATGC CCCTNAAGGC CTCGCTGGAG ATCGAGTACC	60
AAGTTTTAGA TGGAGCAGGA TTAGATATTG ATTTCCCATC TTGCCTCTCC AGAAGGCAAA	120
ACCTTAGTTT TTGAACAAAG AAAATCAGAT GGAGTTCACA CGTGTATAAG AAGTAAAAAT	180
GGGCCAGGCA CTGCGGTTCA CGCCTATAAT CCCAGCACTT TCCGAGGCCG AGTGTAGAGA	240
CTGAAGTTGG TGATTACATG TTCTGCTTTG ACAATACATT CAGCACCATT TCTGAGAAGG	300
TGATTTTCTT TGAATTAATC CTGGATAATA TGGGAGGACA GGCACAAGAC AAGAGGTTTG	360
GAGNATATTT ACTGGCCNAT TTATGGTATG	390

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 530 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGACTCCAGA TTTCCCTGTC AACCACGAGG AGTCCAGAGA GGAAACGCGG AGANGAACAA	60
CAGTACCTGA CGCCTCTTTC AGCCCGGGAT CGCCCCAGCA GGGATGGGCG ACAAGATCTG	120

GCTGCCCTTC	CCCGTGCTCC	TTCTGGCCGC	TCTGCCTCCG	GTGCTGCTGC	CTNGGGNCGG	180
CCGGCTTCAC	ACCTTCCCTC	GATAGCGACT	TCACCTTTAC	CCTTCCCGCC	GGCCAGAAGG	240
AGTGCTTCTA	CCAGCCCATG	CCCCTGAAGG	CCTCGCTGGA	GATCGAGTAC	CAAGTTTTAG	300
ATGGAGCAGG	ATTAGATATT	GATTTCCATC	TTGCCTCTCC	AGAAGGCAAA	ACCTTAGTTT	360
TTGAACAAAG	AAAATCAGAT	GGAGTTCACA	CTGTAGAGAC	TGAAGTTGGT	GATTACATGT	420
TCTGCTTTGA	CAATACATTC	AGCACCATTT	CTGAGAAGGT	GATTTTCTTT	GAATTAATCC	480
TGGATAATAT	GGGAGAACAG	GCACAAGAAC	AAGAAGATTG	GAAGAAATAT		530

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 463 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGACTCCAGA	TTTCCCTGTC	AACCACGAGG	AGTCCAGAGA	GGAAACGCGG	AGCGCACAAC	60
AGTACCTGAC	GCCTCTTTCA	GCCC GGGATC	GCCCCAGCAG	GGATGGGCGA	CAAGATCTGG	120
CTGCCCTTCC	CCGTGCTCCT	TCTGGCCGCT	CTGCCTCCGG	TGCTGCTGCC	TGGGGCGGCC	180
GGCTTCACAC	CTTCCCTCGA	TAGCGACTTC	ACCTTTACCC	TTCCCGCCGG	CCAGAAGGAG	240
TGCTTCTACC	AGCCCATGCC	CCTGAAGGCC	TCGCTGGAGA	TCGAGTACCA	AGTTTTAGAT	300
GGAGCAGGAT	TAGATATTGA	TTTCCATCTT	GCCTCTCCAG	AAGGCAAAAC	CTTAGTTTTT	360
GAACAAAGAA	AATCAGATGG	AGTTCACACT	GTAGAGACTG	AAGTTGGTGA	TTACATGTTC	420
TGCTTTGACA	ATACATTCAG	CACCATTCTT	GAGAAGGTGA	TTT		463

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 196 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCAGAAATATA	GGTTTAACTG	AATGAAGCCA	TATTAATAAC	TGCATTTGCC	TAAC TTGGAA	60
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AAGTTTGGCA AATGTCTTAG GTGATTTAAA TAAATGAGTA TTGGGCCTAA TTGCCACACC	120
AGTCTGTTTT GAACAGGTTT TATTACCCAG AACTTTTTTTG TAAATGCGGC AGTTACAAAT	180
TAAGTGTGG AGGTTT	196

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 520 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCAAAACCTT AGTTTTTGAA CAAAGAAAT CAGATGGAGT TCACACTGTA GAGACTGAAG	60
TTGGTGATTA CATGTTCTGC TTTGACAATA CATTTCAGCAC CATTTCTGAG AAGGTGATTT	120
TCTTTGAATT AATCCTGGAT AATATGGGAG AACAGGCACA AGAACAAGAA GATTGGAAGA	180
AATATATTAC TGGCACAGAT ATATTGGATA TGAAACTGGA AGACATCCTG GAATCCATCA	240
ACAGCATCAA GTCCAGACTA AGCAAAAGTG GGCACATACA AACTCTGCTT AGAGCATTTG	300
AAGCTCGTGA TCGAAACATA CAAGAAAGCA ACTTTGATAG AGTCAATTTC TGGTCTATGG	360
TTAATTTAGT GGTTCATGGT GTGGTGTGAG CCATTCAAGT TTATATGCTG AAGAGTCTGG	420
TTTGAAGATN AGGAGGGAAA GTTGGAAGTT AAAACTCCCA AACTTGGGTA CGGNACCTTG	480
NAAAATGGGG CCATTAAAAA TGCCATTAAC NGGTTCCAGC	520

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 477 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AGACTCCAGA TTTCCCTGTC AACCACGAGG AGTCCAGAGA GGAAACGCGG AGATGAACAA	60
CAGTACCTGA CGCCTCTTTC AGCCCGGGAT CGCCCCAGCA GGGATGGGCG ACAAGATCTG	120
GCTGCCCTTC CCCGTGCTCC TTCTGGCCGC TCTGCCTCCG GTGCTGCTGC CTGGGNGGCC	180
GGCTTCACAC CTTCCCTCGA TAGCGACTTC ACCTTTACCC TTCCCGCCGG CCAGAAGGAG	240

TGCTTCTACC	AGCCCATGCC	CCTGAAGGCC	TCGCTGGAGA	TCGAGTACCA	AGTTTTAGAT	300
GGAGCAGGAT	TAGATATTGA	TTTCCATCTT	GCCTCTCCAG	AAGGCAAAAC	CTTAGTTTTT	360
GAACAAAGAA	AATCAGATGG	GAGTTCACAC	TGTAAGAGAC	TGAAGTTGGG	TGATTACATG	420
TTCTGCTTTG	ACAATACATT	CAGCACCATT	TCTGAGAAGG	TGATTTCTTT	GGAATTA	477

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 403 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTAGTCTAAA	GATTTATTCA	ATCCATCATT	AGGTAATTCT	CAGGTGATTT	ATAACTTAAA	60
ACTGAAAAC	TCCACAGTTA	ATTTGTAAC	GCCGCATTTA	CAAAAAAGTT	CTGGGTAATA	120
GAACCTGTTA	AAAACAGACT	GGTGTTGCAA	TTAGGCCCAA	TACTCATTTA	TTTAAATCAC	180
CTAAGACATT	TGCAAAATTT	TTCAAAGTTA	GGAAAATGCA	GTTATTAATA	TGGCTTCATT	240
CAGTTAAACC	TATATTCTGC	AAAATATTCC	TGTTACACAC	TTAAGGTACA	ACTGGATCAG	300
CAGGATTACT	TGCACAGAAA	GNTGAAGACT	TAATTTTCAC	ATTAAAATTA	TACCTGGTTT	360
CCTACTTTTA	TATCNCAAAA	TATTTTGGGA	GAAGACCATT	AAT		403

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TACCTGACGC	CTCTTTCAGC	CCGGGATCGC	CCCAGCAGGA	ATGGGCGACA	AGATCTGGCT	60
GCCCTTCCCG	TGCTCCTTCT	GGCCGCTCTG	CTCCGGTGCT	GCTGCCTGGG	NGGCCGGCTT	120
CACACCTTCC	CTCGATAGCG	ACTTCACCTT	TACCTTCCGC	CGGCAGAAGG	AGTGCTNCTA	180
CCAGCCATGC	NCCTGAAGGC	CTCNETGGAG	ATCGAGTACC	AAGTTTTAGA	TGGAGCAGGA	240
TTAGATATTG	ATTTCCATCT	TGCCTCTCCA	AGAAAAGGCAA	AACCTTAAGT	TTTTGAACAA	300

AGAAATCAGA TGGAGTTCAC ACTGTAGAGA CTGAAAGTTG GTGATTACAT GTTCTGCTTT	360
GACAATACAT TCAAGAACCA TTTCTGAGAA GGTGAT	396

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCAGAAGGAG TGCTTCTACC AGCCCATGCC CCGTGAAGGC CTCGCTGGAG ATCGAGTACC	60
AAGTTTTAGA TGGAGCAGGA TTAGATATTG ATTTCCATCT TGCCTCTCCA GAAGGCAAAA	120
CCTTAGTTTT TGAACAAAGA AAATCAGATG GAGTTCACAC TGTAGAGACT GAAGTTGGTG	180
ATTACATGTT CTGCTTTGAC AATACATTCA GCACCATTTT TGAGAAGGTG ATTTTCTTTG	240
AATTAATCCT GGATAATATG GGAGAACAAG GCACAAGAAC AAGAAGATTG GAAGAAATAT	300
ATTACTGGC	309

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATTGATTTCC ATCTTGCCCTC TCCAGAAGGC AAAACCTTAG TTTTGAACA AAGAAAATCA	60
GATGGAGTTC AACTGTAGA GACTGAAGTT GGTGATTACA TGTCTGCTT TGACAATACA	120
TTCAGACCA TTTCTGAGAA GGTGATTTTC TTTGAATTAA TCCTGGATAA TATGGGAGAA	180
CAGGCACAAG AACAAGAAGA TTGGAAGAAA TATATTACTG GCACAGATAT ATTGGATATG	240
AAACTGGAAG ACATCCTGGG AATCCATCAA CAGCATCAAG TCCAGACTAA GGCAAAAGTG	300
GGGCACATAC AACTCTGCT TAGGAGCATT TGGAAGGCTC GTGGATCCGA AACATTACAA	360
GGAAAGGCAA CTTTGGATTA GGAGTCCAAT TTCTGGGTCT ATGGGTTAAT TTAGTGGGTC	420
ATGGTGGTGG TGTTCAGCCT TCAGTTTATA TGGCTGGAGG NT	462

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 423 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCGCGGAGAN GGACAACAGT ACCTGACGCC TCTTTCAGCC CGGGATCGCC CCACCAGGGA	60
ATGGGCGACA AGATCTGGCT GCCCTTCCCC GTGCTCCTTC TGGCCGCTCT GCCTCCGGTG	120
CTGCTGCCTG GGGGGCCGGC TTCACACCTT CCCTCGATAG CGACTTCACC TTTACCCTTC	180
CCGCCGGCCA GAAGGAGTGC TTCTACCAGC CCATGCCCCT GAAGGCCTCG CTGGGAGATC	240
GAGTACCAAG TTTTAGATGG AGCAGGATTA GATATTGATT TCCATCTTGC CTCTCCAGAA	300
GGGCAAAACC TTAGTTTTTG GAACAAAGGA AAATCAGGTG GGAGTTTCAC ANTGTAGGAG	360
GATTGAAGTT GGGTGGATTT ACATGTTTCT GGTTTTTGAC AATTACATTT CAGGCACCNT	420
TTT	423

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 450 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGCGGAGACG NATCAACAGT ACCTGACGCC TCTTTCAGCC CCGGATCGCC CCAGCAGGAT	60
TGGGCGACAA GATCTGGCTG CCCTTCCCCG TGCTCCTTCT GGCCGCTCTG CCTCCGGTGC	120
TGCTGCCTGG GGGGCCGGCT TCACACCTTC CCTCGATAGC GACTTCACCT TTACCCTTCC	180
CGCCGGCCAG AAGGAGTGCT TCTACCAGCC CATGCCCCTG AAGGCCTCGC TGGGAGATCG	240
AGTACCAAGT TTTAGATGGG AGCAGGATTA GATATTGATT TTCCATCTTG CCTCTCCAGA	300
AGGGCAAAAC CTTAGTTTTT TGAACAAAGG AAAATCAGGT GGGGAGTTTC ACAATGTAGG	360
AGGATTGAAG TTTGGGTGAT TTACATGTTT TTGCTTTTGA ACAATTACAT TTCAGGCANC	420
ATTTTTGAGG NAGGGTGAAT TTTCTTTGGA	450

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 402 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TAATAACTGC ATTTTCCTAA CTTTGAAAAA TTTTGCAAAT GTCTTAGGTG ATTTAAATAA	60
ATGAGTATTG GGCCTAATTG CAACACCAGT CTGTTTTTAA CAGGTTCTAT TACCCAGAAC	120
TTTTTTGTAA ATGCGGCAGT TACAAATTAA CTGTGGAAGT TTTCAGTTTT AAGTTATAAA	180
TCACCTGAGA ATTACCTAAT GATGGATTGA ATAAATCTTT AGACTACAAA AGCCCAACTT	240
TTCTCTATTT ACATATGCAT CTCTCCTATA ATGTAAATAG AATAATAGCT TTGAAATACA	300
ATTAGGTTTT TGAGATTTTT ATAACCAAAT ACATTTTCAGT GTAACATATT AGCAGAAAGC	360
ATTAGTCCTT GGACTTTGCT TACATTCCCA AAAGCTGACA TT	402

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTCCATCTTG CCTCTCCAGA AGGCAAAACC TTAGTTTTTG AACAAAGAAA ATCAGATGGA	60
G TTCACACTG TAGAGACTGA AGTTGGTGAT TACATGTTCT GCTTTGACAA TACATTCAGC	120
ACCATTTCTG AGAAGGTGAT TTTCTTTGAA TTAATCCTGG ATAATATGGG AGAACAGGCA	180
CAGGAACAAG AGGATTGGGA GGAATATATT ACTGGCACAG ATATATTGGA TATGAACTGG	240
AGACATCTGG ATCATCACAG CATCAGTCCA GACTAGCAAA GTGGGCACAT CAACTCTCTT	300
AGGCATTTG	309

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 286 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGACTCCAGA	TTTCCCTGTC	AACCACGAGG	AGTCCAGAGA	GAAAACGCGG	AGATGAGCAA	60
GCAGTACCTG	ACGCCCTCTT	CAGCCCGGGA	TCGCCCCAGC	AGGGATGGGC	GACAAGATCT	120
GGCTGCCCTT	CCCCGTGCTC	CTTCTGGCCG	CTCTGCCTCC	GGTGCTGCTG	CCTGGGCGGC	180
CGGCTTCACA	CCTTCCCTCG	ATAGCGACTT	CACCTTTACC	CTTCCCGCCG	GCCAGAAGGA	240
GTGCTTCTAC	CAGCCCATGC	GCCTGAAAGC	CTCTCTTGAG	ATCGAG		286

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